



PCT09

RAW SEQUENCE LISTING

DATE: 08/01/2002

PATENT APPLICATION: US/09/763,129B

TIME: 20:27:32

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ENTERED

1 <110> APPLICANT: CO, MAN SUNG
 2 MAXIMILLIANO, VASQUEZ
 3 <120> TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
 FACTOR MONOCLONAL

4 ANTIBODY
 5 <130> FILE REFERENCE: 202617US0PCT
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/763,129B
 7 <141> CURRENT FILING DATE: 2002-07-01
 8 <150> PRIOR APPLICATION NUMBER: PCT/US99/16724
 9 <151> PRIOR FILING DATE: 1999-08-19
 10 <150> PRIOR APPLICATION NUMBER: 09/136,315
 11 <151> PRIOR FILING DATE: 1998-08-19
 12 <160> NUMBER OF SEQ ID NOS: 8
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 417
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Mus musculus
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (1)..(417)
 22 <223> OTHER INFORMATION:
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25	Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val	
26	1 5 10 15	
27	cag tgt gag gtg aaa ctt ctc gag tct gga ggt ggc ctg gtg cag act	96
28	Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr	
29	20 25 30	
30	gga gga tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt	144
31	Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser	
32	35 40 45	
33	aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa	192
34	Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu	
35	50 55 60	
36	tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca	240
37	Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro	
38	65 70 75 80	
39	tct cta aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg	288
40	Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr	
41	85 90 95	
42	ctg tac ctg caa atg agt caa gtg aga tct gag gac aca gcc ctt tac	336
43	Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr	
44	100 105 110	

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45      tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac      384
46      Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
47          115                      120                      125
48      tgg ggc caa ggg act ctg gtc tct gtc tcg cca      417
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59      Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
60          20                      25                      30
61      Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
62          35                      40                      45
63      Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
64          50                      55                      60
65      Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
66          65                      70                      75                      80
67      Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
68          85                      90                      95
69      Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
70          100                     105                     110
71      Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
72          115                     120                     125
73      Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
74          130                     135
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79 <213> ORGANISM: Mus musculus
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83 <223> OTHER INFORMATION:
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87          1                      5                      10                      15
88      gat gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct      96
89      Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
90          20                      25                      30
91      gta tct gtg gga gaa act gtc acc atc aca tgt cga gca agt gag aat      144
92      Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
93          35                      40                      45
94      att tac aat aat tta gct tgg tat cag cag aga cag gga aaa tct cct      192
95      Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro

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98  Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
99  65          70          75          80
100  agg ttc agt ggc agt gga tca ggc aca cag tat tcc ctc aag atc gac      288
101  Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
102          85          90          95
103  agc ctg cag tct gaa gat ttt ggg agt tat tac tgt caa cat ttg tgg      336
104  Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
105          100          105          110
106  act tct ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa      381
107  Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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111 <211> LENGTH: 127
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113 <213> ORGANISM: Mus musculus
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118          20          25          30
119  Val Ser Val Gly Glu Thr Val Thr Thr Cys Arg Ala Ser Glu Asn
120          35          40          45
121  Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
122          50          55          60
123  Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
124          65          70          75          80
125  Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
126          85          90          95
127  Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
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129  Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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133 <211> LENGTH: 417
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135 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
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140 <222> LOCATION: (1)..(417)
141 <223> OTHER INFORMATION:
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144  Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
145  1          5          10          15
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150      Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
151              35                      40                      45
152      aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg ctc gag      192
153      Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
154              50                      55                      60
155      tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca      240
156      Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
157      65                      70                      75                      80
158      tct cta aag gat aaa ttc acc atc tcc aga gac aac gcc aaa aat acg      288
159      Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
160              85                      90                      95
161      ctg tac ctg caa atg aac tca ttg aga gct gag gac acg gcc gtt tac      336
162      Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
163              100                     105                     110
164      tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac      384
165      Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
166              115                     120                     125
167      tgg ggc caa ggg act ctg gtc acc gtc tcc tca      417
168      Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
169              130                     135
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172 <211> LENGTH: 139
173 <212> TYPE: PRT
174 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Synthetic Peptide
177 <400> SEQUENCE: 6
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181              20              25              30
182      Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
183              35              40              45
184      Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
185              50              55              60
186      Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
187      65              70              75              80
188      Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
189              85              90              95
190      Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
191              100             105             110
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RAW SEQUENCE LISTING

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205 <222> LOCATION: (1)..(381)
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210   1           5           10           15
211   gat gcc aga tgt gac atc cag atg act cag tct cca tcc tcc cta tct      96
212   Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
213   20           25           30
214   gca tct gtg gga gac agg gtc acc atc aca tgt cga gca agt gag aat      144
215   Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
216   35           40           45
217   att tac aat aat tta gct tgg tat cag cag aaa ccg gga aaa gct cct      192
218   Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
219   50           55           60
220   aag cta cta gtc tat gct gca aca aac tta gca gat ggt gtg cca tca      240
221   Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
222   65           70           75           80
223   agg ttc agt ggc agt gga tca ggc aca cag tat acc ctc acg atc agc      288
224   Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
225   85           90           95
226   agc ctc cag cct gag gat ttt gcg act tat tac tgt caa cat ttg tgg      336
227   Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp
228   100          105          110
229   act tct ccg tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa      381
230   Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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243   20           25           30
244   Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
245   35           40           45
246   Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
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VERIFICATION SUMMARY

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